

## SEQUENCE LISTING

945  
5  
(1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: MOGEN International nv  
(B) STREET: Einsteinweg 97  
(C) CITY: Leiden  
10 (E) COUNTRY: The Netherlands  
(F) POSTAL CODE (ZIP): 2333 CB  
(G) TELEPHONE: 31-(0)71-5258282  
(H) TELEFAX: 31-(0)71-5221471

15

(A) NAME: Gist-brocades N.V.  
(B) STREET: Postbus 1

(C) CITY: Delft  
(E) COUNTRY: The Netherlands  
(F) POSTAL CODE (ZIP): 2600 MA  
(G) TELEPHONE: 31-(0)15-2799111  
20 (H) TELEFAX: 31-(0)15-2793957

25

(ii) TITLE OF INVENTION: Improved process for the production of  
alcoholic beverages using Maltseed

30

(iii) NUMBER OF SEQUENCES: 8

35

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
40 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

45

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 96202195.2  
(B) FILING DATE: 05-AUG-1996

## (2) INFORMATION FOR SEQ ID NO: 1:

50

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
45 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

60

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..558

(D) OTHER INFORMATION: /product= "mature protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

5	ATG AGC GCG GGA ATC AAC TAC GTC CAG AAC TAC AAT GGC AAC CTC GGC Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly 1 5 10 15	48
10	GAC TTT ACT TAC GAC GAG TCA GCG GGA ACT TTC AGC ATG TAT TGG GAG Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu 20 25 30	96
15	GAT GGC GTG TCC TCA GAC TTC GTC GTG GGA CTG GGC TGG ACC ACT GGA Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly 35 40 45	144
20	TCA TCC AAT GCG ATC ACC TAC AGC GCC GAG TAC TCC GCG TCA GGA TCA Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser 50 55 60	192
25	GCC TCC TAT CTG GCC GTG TAC GGA TGG GTG AAC TAC CCG CAG GCC GAG Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu 65 70 75 80	240
30	TAC TAC ATC GTG GAG GAT TAC GGA GAT TAC AAC CCA TGC AGC TCA GCG Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala 85 90 95	288
35	ACC TCC CTC GGA ACT GTG TAC AGC GAC GGC TCC ACC TAC CAG GTC TGC Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys 100 105 110	336
40	ACC GAC ACC CGC ACT AAC GAG CCG TCA ATC ACC GGC ACT TCC ACC TTC Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe 115 120 125	384
45	ACC CAG TAC TTC AGC GTG CGC GAG TCC ACT CGC ACC TCA GGA ACC GTG Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val 130 135 140	432
50	ACC GTC GCG AAC CAC TTC AAC TTC TGG GCG CAG CAC GGA TTC GGC AAC Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn 145 150 155 160	480
55	AGC GAC TTT AAC TAC CAG GTG GTC GCA GTG GAG GCA TGG TCA GGA GCG Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala 165 170 175	528
60	GGC TCA GCG TCC GTC ACT ATC AGC TCC TG Gly Ser Ala Ser Val Thr Ile Ser Ser 180 185	558

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 185 amino acids  
(B) TYPE: amino acid  
(C) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

## 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly  
1 5 10 15

20 Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu  
20 25 30

Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly  
35 40 45

25 Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser  
50 55 60

30 Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu  
65 70 75 80

35 Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala  
85 90 95

40 Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys  
100 105 110

45 Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe  
115 120 125

50 Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val  
130 135 140

55 Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn  
145 150 155 160

60 Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala  
165 170 175

65 Gly Ser Ala Ser Val Thr Ile Ser Ser  
180 185

## (2) INFORMATION FOR SEQ ID NO: 3:

## 50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

*b7*  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Nicotiana tabacum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AACTTCCTCA AGAGCTTCCC CTTTTATGCC TTCCTTGTT TTGGCCAATA CTTTGTAGCT 60

15 GTTACGCATG C

71

(2) INFORMATION FOR SEQ ID NO: 4:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30 (iii) HYPOTHETICAL: NO

35 (iii) ANTI-SENSE: YES

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCATGGCATG CGTAACAGCT ACAAAAGTATT GGCCAAAACA AAGGAAGGCA TAAAAGGGGA 60

45 AGCTCTTGAG GAAGTTCATG 80

(2) INFORMATION FOR SEQ ID NO: 5:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (iii) HYPOTHETICAL: NO

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGGATGGCA TGCTGTTGTA G

21

B4  
(2) INFORMATION FOR SEQ ID NO: 6:

5  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10  
(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

15  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCACAATTCT CGAGGAGACC G

21

## (2) INFORMATION FOR SEQ ID NO: 7:

20  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25  
(ii) MOLECULE TYPE: cDNA

30  
(iii) HYPOTHETICAL: NO

35  
(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

40  
CCTCTTAAGG ATCCAATGCG G

21

## (2) INFORMATION FOR SEQ ID NO: 8:

45  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50  
(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

55  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

60  
CTTATCTGAA TTCGGAAGCT C

21